

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	6646588	reduce or reduction or diminish or diminution or decrease or decreased or diminished or reduced	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L2	13851	(factor adj (viii or viiiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L3	2083665	mutant or mutated or modified or variant or analog or allele	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L4	67125	(T adj cell) or T-cell or thymocyte or T-helper	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L5	599063	antigenicity or immunogenicity or reactivity or antigenic or immunogenic or reactive	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:44
L6	4	L1 same L4 same L5 same L2 same L3	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:46
L7	132	(L1 with L5) and (L2 same L3) and L4	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L8	27	((L1 with L5) same L4) and (L2 same L3)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L9	13851	(factor adj (viii or viiiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L10	211	jacquemin.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47
L11	11	L10 and L9	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:47

EAST Search History

L12	49340	jones.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L13	13851	(factor adj (viii or viiiia or eight or "8")) or fviii or fviiia	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L14	76	L12 and L13	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48
L15	29	L14 and (L1 same L5)	US-PGPUB; USPAT; EPO; JPO; DERWENT	ADJ	ON	2006/06/16 11:48

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559- 73.rag.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:48:54 ; Search time 211 Seconds
(without alignments)
3116.006 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRYYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	7693	100.0	1438	7	ADM75983	Adm75983 Wild-type
2	7693	100.0	1457	2	AAW46246	Aaw46246 Human fac
3	7693	100.0	1457	2	AAW44372	Aaw44372 Human Fac
4	7693	100.0	1457	8	ADU47569	Adu47569 Human fac
5	7688	99.9	1438	7	ADM75988	Adm75988 Modified
6	7688	99.9	1438	7	ADM75985	Adm75985 Modified
7	7688	99.9	1438	7	ADM75989	Adm75989 Modified
8	7688	99.9	1438	7	ADM75984	Adm75984 Modified
9	7687	99.9	1438	7	ADM75986	Adm75986 Modified
10	7687	99.9	1438	7	ADM75987	Adm75987 Modified
11	7684	99.9	1438	3	AAB01262	Aab01262 B-domain
12	7684	99.9	1438	7	ADF31316	Adf31316 Variant o
13	7684	99.9	1457	2	AAY21675	Aay21675 Beta-doma
14	7684	99.9	1457	7	ADM98124	Adm98124 Human fac
15	7679.5	99.8	1464	8	ADU47624	Adu47624 Human fac
16	7676	99.8	1471	8	ADU47625	Adu47625 Human fac
17	7672	99.7	1479	8	ADU47617	Adu47617 Human fac
18	7668.5	99.7	1440	2	AAR12971	Aar12971 Factor VI
19	7667	99.7	1471	2	AAW23414	Aaw23414 Human B-d
20	7667	99.7	1471	4	AAB67959	Aab67959 Amino aci
21	7666	99.6	1471	8	ADU47608	Adu47608 Human fac
22	7637	99.3	1455	8	ADU47609	Adu47609 Human fac
23	7637	99.3	1461	8	ADU47616	Adu47616 Human fac
24	7635	99.2	1459	4	AAE10832	Aae10832 Human fac
25	7627.5	99.1	1568	8	ADU47621	Adu47621 Human fac
26	7625	99.1	1440	8	ADQ37592	Adq37592 Human Fac
27	7625	99.1	1459	4	AAE10833	Aae10833 Human fac
28	7622	99.1	1459	4	AAE10827	Aae10827 Human fac
29	7620.5	99.1	1516	1	AAP80265	Aap80265 Modified
30	7619	99.0	1585	8	ADU47607	Adu47607 Human fac
31	7619	99.0	1585	8	ADU47613	Adu47613 Human fac
32	7614.5	99.0	1447	8	ADQ37595	Adq37595 Human Fac
33	7614	99.0	1428	8	ADQ37589	Adq37589 Human Fac
34	7614	99.0	1440	8	ADQ37607	Adq37607 Human Fac
35	7610	98.9	1453	8	ADU47619	Adu47619 Human fac
36	7604.5	98.8	1450	8	ADU47615	Adu47615 Human fac
37	7603.5	98.8	1437	8	ADQ37593	Adq37593 Human Fac
38	7603.5	98.8	1447	8	ADQ37610	Adq37610 Human Fac
39	7603	98.8	1428	8	ADQ37604	Adq37604 Human Fac
40	7603	98.8	1444	8	ADQ37596	Adq37596 Human Fac
41	7603	98.8	1457	8	ADU47622	Adu47622 Human fac
42	7601	98.8	1424	4	AAB48842	Aab48842 Mutant ma
43	7601	98.8	1424	5	AAO18622	Aao18622 Human mat
44	7601	98.8	1424	9	ADZ65051	Adz65051 Human mat
45	7599.5	98.8	1441	8	ADQ37597	Adq37597 Human Fac

ALIGNMENTS

RESULT 1
ADM75983
ID ADM75983 standard; protein; 1438 AA.
XX
AC ADM75983;
XX
DT 03-JUN-2004 (first entry)

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559-73.i

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:59:22 ; Search time 56 Seconds
(without alignments)
2247.661 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATRRYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	7693	100.0	1457	2	US-09-001-039B-47	Sequence 47, Appl

2	7684	99.9	1438	2	US-09-209-916-1	Sequence 1, Appli
3	7667	99.7	1471	1	US-08-683-839B-3	Sequence 3, Appli
4	7597	98.8	1447	2	US-09-407-605-4	Sequence 4, Appli
5	7587	98.6	1445	2	US-09-407-605-3	Sequence 3, Appli
6	7443	96.8	1661	1	US-08-882-083-2	Sequence 2, Appli
7	7443	96.8	1661	1	US-08-558-107-2	Sequence 2, Appli
8	7443	96.8	1661	2	US-09-243-539-2	Sequence 2, Appli
9	7236	94.1	2332	2	US-10-360-101-229	Sequence 229, App
10	7236	94.1	2351	1	US-08-366-851A-2	Sequence 2, Appli
11	7236	94.1	2351	2	US-10-133-907-4	Sequence 4, Appli
12	7236	94.1	2351	2	US-09-001-039B-45	Sequence 45, Appli
13	7233	94.0	2332	1	US-08-276-594A-2	Sequence 2, Appli
14	7230	94.0	2351	7	5171844-2	Patent No. 5171844
15	7227	93.9	2332	1	US-07-864-004B-4	Sequence 4, Appli
16	7227	93.9	2332	1	US-08-251-937A-4	Sequence 4, Appli
17	7227	93.9	2332	1	US-08-212-133A-2	Sequence 2, Appli
18	7227	93.9	2332	1	US-08-474-503-2	Sequence 2, Appli
19	7227	93.9	2332	1	US-08-670-707A-2	Sequence 2, Appli
20	7227	93.9	2332	2	US-09-037-601-2	Sequence 2, Appli
21	7227	93.9	2332	2	US-09-315-179-2	Sequence 2, Appli
22	7227	93.9	2332	2	US-09-523-656-2	Sequence 2, Appli
23	7227	93.9	2332	2	US-09-957-641A-2	Sequence 2, Appli
24	7227	93.9	2332	3	US-10-187-319-2	Sequence 2, Appli
25	7227	93.9	2332	3	US-10-131-510A-2	Sequence 2, Appli
26	7227	93.9	2332	5	PCT-US93-03275-4	Sequence 4, Appli
27	7227	93.9	2332	5	PCT-US94-13200-2	Sequence 2, Appli
28	7227	93.9	2351	1	US-08-121-202-2	Sequence 2, Appli
29	7218	93.8	2351	7	5422260-1	Patent No. 5422260
30	7188	93.4	2332	2	US-09-324-867-3	Sequence 3, Appli
31	6569	85.4	1467	2	US-09-523-656-38	Sequence 38, Appli
32	6498	84.5	1443	1	US-08-670-707A-39	Sequence 39, Appli
33	6498	84.5	1443	2	US-09-037-601-39	Sequence 39, Appli
34	6498	84.5	1443	2	US-09-315-179-39	Sequence 39, Appli
35	6498	84.5	1443	3	US-10-187-319-39	Sequence 39, Appli
36	6498	84.5	1443	3	US-10-131-510A-39	Sequence 39, Appli
37	6281	81.6	2343	2	US-09-324-867-2	Sequence 2, Appli
38	6236	81.1	2133	1	US-08-670-707A-37	Sequence 37, Appli
39	6236	81.1	2133	2	US-09-037-601-37	Sequence 37, Appli
40	6236	81.1	2133	2	US-09-315-179-37	Sequence 37, Appli
41	6236	81.1	2133	2	US-09-523-656-30	Sequence 30, Appli
42	6236	81.1	2133	3	US-10-187-319-37	Sequence 37, Appli
43	6236	81.1	2133	3	US-10-131-510A-37	Sequence 37, Appli
44	6201	80.6	2319	1	US-08-212-133A-8	Sequence 8, Appli
45	6201	80.6	2319	1	US-08-474-503-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-001-039B-47

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; Sequence 47, Application US/09001039B
; Patent No. 6818439
; GENERAL INFORMATION:
; APPLICANT: Jolly, Douglas J.
; APPLICANT: Chang, Stephen M.W.
; APPLICANT: Respass, James G.
; APPLICANT: DePolo, Nicholas J.
; APPLICANT: Hsu, David Chi-Tang
; APPLICANT: Ibanez, Carlos E.
; APPLICANT: Greengard, Judith
```

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559- 73.rapbm.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:11:10 ; Search time 205 Seconds
(without alignments)
3249.283 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
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Scoring table: BLOSUM62
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Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	SUMMARIES				Description
		Match	Length	DB	ID	
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2	7684	99.9	1438	4	US-10-006-091-1	Sequence 1, Appli
3	7684	99.9	1438	4	US-10-047-257-1	Sequence 1, Appli
4	7684	99.9	1438	4	US-10-225-900-1	Sequence 1, Appli
5	7684	99.9	1457	5	US-10-813-507-13	Sequence 13, Appl
6	7667	99.7	1471	4	US-10-095-718-2	Sequence 2, Appli
7	7667	99.7	1471	4	US-10-681-970-2	Sequence 2, Appli
8	7635	99.2	1459	4	US-10-239-498A-13	Sequence 13, Appl
9	7625	99.1	1459	4	US-10-239-498A-15	Sequence 15, Appl
10	7622	99.1	1459	4	US-10-239-498A-4	Sequence 4, Appli
11	7601	98.8	1424	5	US-10-472-516-5	Sequence 5, Appli
12	7601	98.8	1424	5	US-10-968-286-5	Sequence 5, Appli
13	7282	94.7	1457	5	US-10-813-507-17	Sequence 17, Appl
14	7236	94.1	2332	4	US-10-360-101-229	Sequence 229, App
15	7236	94.1	2332	4	US-10-466-998A-1	Sequence 1, Appli
16	7236	94.1	2332	4	US-10-721-997A-34	Sequence 34, Appl
17	7236	94.1	2332	5	US-10-789-956-2	Sequence 2, Appli
18	7236	94.1	2351	4	US-10-132-829-4	Sequence 4, Appli
19	7236	94.1	2351	4	US-10-172-712-27	Sequence 27, Appl
20	7236	94.1	2351	4	US-10-133-907-4	Sequence 4, Appli
21	7236	94.1	2351	4	US-10-411-037-30	Sequence 30, Appl
22	7236	94.1	2351	4	US-10-411-026-30	Sequence 30, Appl
23	7236	94.1	2351	4	US-10-410-962-30	Sequence 30, Appl
24	7236	94.1	2351	4	US-10-411-049-30	Sequence 30, Appl
25	7236	94.1	2351	4	US-10-410-930-30	Sequence 30, Appl
26	7236	94.1	2351	4	US-10-410-997-30	Sequence 30, Appl
27	7236	94.1	2351	4	US-10-411-012-30	Sequence 30, Appl
28	7236	94.1	2351	4	US-10-287-994-30	Sequence 30, Appl
29	7236	94.1	2351	4	US-10-410-913-30	Sequence 30, Appl
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31	7236	94.1	2351	5	US-10-472-516-2	Sequence 2, Appli
32	7236	94.1	2351	5	US-10-410-980-30	Sequence 30, Appl
33	7236	94.1	2351	5	US-10-410-897-30	Sequence 30, Appl
34	7236	94.1	2351	5	US-10-968-286-2	Sequence 2, Appli
35	7236	94.1	2351	5	US-10-492-261-30	Sequence 30, Appl
36	7236	94.1	2351	6	US-11-183-205-30	Sequence 30, Appl
37	7236	94.1	2351	6	US-11-244-087-3	Sequence 3, Appli
38	7236	94.1	2351	6	US-11-267-631-49	Sequence 49, Appl
39	7227	93.9	2332	3	US-09-957-641-2	Sequence 2, Appli
40	7227	93.9	2332	4	US-10-187-319-2	Sequence 2, Appli
41	7227	93.9	2332	4	US-10-131-510A-2	Sequence 2, Appli
42	7227	93.9	2332	4	US-10-445-235-2	Sequence 2, Appli
43	7227	93.9	2332	4	US-10-239-498A-2	Sequence 2, Appli
44	7227	93.9	2332	4	US-10-353-753-1	Sequence 1, Appli
45	7227	93.9	2332	5	US-10-491-464-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
 US-10-511-559-73
 ; Sequence 73, Application US/10511559
 ; Publication No. US20050256304A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JONES, Tim
 ; APPLICANT: BAKER, Matthew
 ; APPLICANT: CARR, Francis, J.
 ; TITLE OF INVENTION: MODIFIED FACTOR VIII
 ; FILE REFERENCE: MER-133
 ; CURRENT APPLICATION NUMBER: US/10/511,559

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:12:02 ; Search time 16 Seconds
(without alignments)
1000.968 Million cell updates/sec

Title: US-10-511-559-73
Perfect score: 7693
Sequence: 1 ATTRYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
						%	
1	7693	100.0	1457	7	US-11-280-757-37		Sequence 37, Appl

2	7236	94.1	2351	7	US-11-183-218-30	Sequence 30, Appl
3	7236	94.1	2351	7	US-11-280-757-35	Sequence 35, Appl
4	588	7.6	379	7	US-11-293-697-3405	Sequence 3405, Ap
5	285.5	3.7	524	7	US-11-293-697-3442	Sequence 3442, Ap
6	217	2.8	734	7	US-11-242-505A-24	Sequence 24, Appl
7	212	2.8	734	6	US-10-196-749-458	Sequence 458, App
8	136	1.8	370	7	US-11-293-697-4818	Sequence 4818, Ap
9	122	1.6	364	6	US-10-505-928-605	Sequence 605, App
10	121	1.6	5738	6	US-10-505-928-150	Sequence 150, App
11	119.5	1.6	540	6	US-10-953-349-22757	Sequence 22757, A
12	109	1.4	1575	6	US-10-505-928-257	Sequence 257, App
13	106	1.4	961	6	US-10-548-484-76	Sequence 76, Appl
14	102.5	1.3	735	6	US-10-953-349-5895	Sequence 5895, Ap
15	102.5	1.3	765	6	US-10-953-349-5894	Sequence 5894, Ap
16	102.5	1.3	821	6	US-10-953-349-5893	Sequence 5893, Ap
17	102	1.3	3882	6	US-10-953-349-5549	Sequence 5549, Ap
18	102	1.3	3978	6	US-10-953-349-5548	Sequence 5548, Ap
19	102	1.3	4118	6	US-10-953-349-5547	Sequence 5547, Ap
20	100.5	1.3	690	6	US-10-953-349-1493	Sequence 1493, Ap
21	100.5	1.3	729	6	US-10-953-349-1492	Sequence 1492, Ap
22	100.5	1.3	735	6	US-10-953-349-1491	Sequence 1491, Ap
23	99.5	1.3	541	6	US-10-953-349-8820	Sequence 8820, Ap
24	99.5	1.3	544	6	US-10-953-349-2547	Sequence 2547, Ap
25	99.5	1.3	546	6	US-10-953-349-2546	Sequence 2546, Ap
26	99.5	1.3	592	6	US-10-953-349-3845	Sequence 3845, Ap
27	99.5	1.3	1534	6	US-10-505-928-40	Sequence 40, Appl
28	99	1.3	495	6	US-10-953-349-6931	Sequence 6931, Ap
29	99	1.3	497	6	US-10-953-349-6930	Sequence 6930, Ap
30	99	1.3	507	6	US-10-953-349-6929	Sequence 6929, Ap
31	99	1.3	666	6	US-10-953-349-24660	Sequence 24660, A
32	99	1.3	696	6	US-10-953-349-24659	Sequence 24659, A
33	99	1.3	716	6	US-10-953-349-24658	Sequence 24658, A
34	98	1.3	698	7	US-11-293-697-4312	Sequence 4312, Ap
35	97	1.3	329	6	US-10-953-349-16881	Sequence 16881, A
36	96.5	1.3	591	7	US-11-045-540-1	Sequence 1, Appli
37	96.5	1.3	670	7	US-11-121-154-59	Sequence 59, Appl
38	96.5	1.3	1194	7	US-11-045-540-2	Sequence 2, Appli
39	96.5	1.3	1205	7	US-11-045-540-3	Sequence 3, Appli
40	96.5	1.3	1237	7	US-11-045-540-4	Sequence 4, Appli
41	96.5	1.3	1248	7	US-11-045-540-5	Sequence 5, Appli
42	96	1.2	1344	7	US-11-314-018-20	Sequence 20, Appl
43	96	1.2	1531	6	US-10-505-928-217	Sequence 217, App
44	95.5	1.2	566	6	US-10-548-484-83	Sequence 83, Appl
45	95	1.2	1042	6	US-10-548-484-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-11-280-757-37

; Sequence 37, Application US/11280757

; Publication No. US20060099685A1

; GENERAL INFORMATION:

; APPLICANT: Crucell Holland B.V.

; APPLICANT: Bout, Abraham

; APPLICANT: Opstelten, Dirk-Jan

; APPLICANT: Yallop, Christopher

; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF FACTOR VIII IN HUMAN CELLS

; FILE REFERENCE: 0034 D US P00 CIP

; CURRENT APPLICATION NUMBER: US/11/280,757

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:52:56 ; Search time 53 Seconds
(without alignments)
2610.560 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRRYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Query				Description
	Score	Match	Length	DB	

1	7236	94.1	2351	1	EZHU	coagulation factor
2	6236	81.1	2133	2	T42763	coagulation factor
3	6201	80.6	2319	2	A47004	coagulation factor
4	2391.5	31.1	2224	1	KFHU5	coagulation factor
5	2371	30.8	2183	2	T42764	coagulation factor
6	2370	30.8	2211	1	KFB05	coagulation factor
7	1740.5	22.6	1069	1	KUHU	ferroxidase (EC 1.)
8	1696.5	22.1	1059	1	A35210	ferroxidase (EC 1.)

9	1104	14.4	216	2	A44258	factor VIII-associ
10	663	8.6	427	2	JC4915	ags protein precur
11	657	8.5	463	1	A36479	milk fat globule m
12	650	8.4	409	2	T11743	pP47 protein - pig
13	635	8.3	401	2	S65138	glycoprotein antig
14	635	8.3	427	2	S74211	PAS-6/7 protein pr
15	543	7.1	869	2	A25945	coagulation factor
16	443	5.8	927	1	JQ0948	A5 antigen precurs
17	424.5	5.5	218	2	A47285	milk fat globule p
18	306.5	4.0	3133	2	S52093	hemocytin - silkwo
19	262	3.4	845	2	JC5256	adipocyte transcri
20	221	2.9	719	2	S51739	transcription repr
21	211	2.7	1283	2	T13799	neurexin IV - frui
22	207.5	2.7	737	2	T31349	hypothetical prote
23	206.5	2.7	737	2	T15615	hypothetical prote
24	193	2.5	913	2	A48280	receptor tyrosine
25	192	2.5	876	2	A49508	protein-tyrosine k
26	185.5	2.4	855	2	S42621	protein-tyrosine k
27	185.5	2.4	910	2	A53137	tyrosine kinase re
28	173.5	2.3	819	2	I48859	tyro 10 receptor k
29	171	2.2	1381	2	T31083	paranodin - rat
30	171	2.2	1385	2	T14158	neurexin IV - mous
31	149.5	1.9	578	2	S66353	L-ascorbate oxidas
32	149	1.9	1883	2	G82875	hypothetical prote
33	148	1.9	622	2	S62580	probable multicopp
34	141.5	1.8	1196	2	S46430	botulinum neurotox
35	140.5	1.8	1196	2	JQ1467	toxin, nontoxic co
36	140.5	1.8	1217	2	T18209	mnxG protein - Bac
37	139	1.8	1193	2	JC4901	nontoxic-nonhemagg
38	137.5	1.8	580	2	F84828	probable laccase (
39	137.5	1.8	903	2	F82080	preprotein translo
40	136.5	1.8	2657	2	T18497	hypothetical prote
41	135	1.8	343	2	T35030	probable copper ox
42	134.5	1.7	791	2	T16031	hypothetical prote
43	134.5	1.7	1132	2	H82887	hypothetical prote
44	133.5	1.7	567	2	T44928	L-ascorbate oxidas
45	133.5	1.7	2925	2	T00133	RNA-directed RNA p

ALIGNMENTS

RESULT 1

EZHU

coagulation factor VIII precursor [validated] - human
 N;Alternate names: antihemophilic factor A; coagulation factor VIIIC; procoagulant com
 C;Species: Homo sapiens (man)
 C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 31-Dec-2004
 C;Accession: I54318; A00525; I58059; A23584; A26174; A42348; A43986; S63527; S66445; B
 R;Gitschier, J.; Wood, W.I.
 Hum. Mol. Genet. 1, 199-200, 1992
 A;Title: Sequence of the exon-containing regions of the human factor VIII gene.
 A;Reference number: I54318; MUID:93265012; PMID:1303178
 A;Accession: I54318
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-1921, 'S', 1923-2351
 A;Cross-references: UNIPROT:P00451; UNIPARC:UPI000016A8D3; GB:M88648; NID:g182381; PID
 R;Wood, W.I.; Capon, D.J.; Simonsen, C.C.; Eaton, D.L.; Gitschier, J.; Keyt, B.; Seebu
 Nature 312, 330-337, 1984
 A;Title: Expression of active human factor VIII from recombinant DNA clones.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 10:48:58 ; Search time 335 Seconds
(without alignments)
3970.664 Million cell updates/sec

Title: US-10-511-559-73

Perfect score: 7693

Sequence: 1 ATRRYYLGAVELSWDYMQSD.....WVHQIALRMEVLGCEAQDLY 1438

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	7236	94.1	2351	1	FA8_HUMAN	P00451 h coagulati
2	7236	94.1	2351	2	Q5HY69_HUMAN	Q5hy69 homo sapien
3	6281	81.6	2343	1	FA8_CANFA	O18806 canis famil
4	6236	81.1	2133	1	FA8_PIG	P12263 sus scrofa

5	6201	80.6	2319	1	FA8_MOUSE	Q06194 mus musculu
6	4967.5	64.6	2258	2	Q7TN96_RAT	Q7tn96 rattus norv
7	3236	42.1	1639	2	Q804W6_FUGRU	Q804w6 fugu rubrip
8	2672.5	34.7	1459	2	Q593B6_PSETE	Q593b6 pseudonaja
9	2652	34.5	1460	2	Q7SZN0_PSETE	Q7szn0 pseudonaja
10	2650.5	34.5	1459	2	Q58L91_9SAUR	Q58191 oxyuranus s
11	2641	34.3	1458	2	Q49MF1_OXYSC	Q49mf1 oxyuranus s
12	2631	34.2	1460	2	Q58L90_OXYMI	Q58190 oxyuranus m
13	2542	33.0	1802	2	Q804W5_FUGRU	Q804w5 fugu rubrip
14	2490.5	32.4	2119	2	Q90X47_BRARE	Q90x47 brachydanio
15	2394.5	31.1	2224	1	FA5_HUMAN	P12259 homo sapien
16	2387.5	31.0	2224	2	Q5R347_HUMAN	Q5r347 homo sapien
17	2380	30.9	1304	2	Q4RPE7_TETNG	Q4rpe7 tetraodon n
18	2375	30.9	2229	2	Q5R346_HUMAN	Q5r346 homo sapien
19	2371	30.8	2183	2	O88783_MOUSE	O88783 mus musculu
20	2370	30.8	2211	1	FA5_BOVIN	Q28107 bos taurus
21	2355.5	30.6	2258	1	FA5_PIG	Q9glp1 sus scrofa
22	2326.5	30.2	1377	2	Q804X3_CHICK	Q804x3 gallus gall
23	2093	27.2	1725	2	Q4S9Q1_TETNG	Q4s9q1 tetraodon n
24	1809	23.5	1157	1	HEPH_MOUSE	Q9z0z4 mus musculu
25	1793	23.3	1157	1	HEPH_RAT	Q920h8 rattus norv
26	1751	22.8	1158	1	HEPH_HUMAN	Q9bqs7 homo sapien
27	1751	22.8	1158	2	Q5JUU0_HUMAN	Q5juu0 homo sapien
28	1740	22.6	1087	2	Q7ZU12_BRARE	Q7zu12 brachydanio
29	1739	22.6	1087	2	Q6P3G1_BRARE	Q6p3g1 brachydanio
30	1736.5	22.6	1065	1	CERU_HUMAN	P00450 homo sapien
31	1736.5	22.6	1065	2	Q2PP18_HUMAN	Q2pp18 homo sapien
32	1718.5	22.3	1084	2	Q9JL97_RAT	Q9jl97 rattus norv
33	1696	22.0	1048	2	Q4T8Z9_TETNG	Q4t8z9 tetraodon n
34	1693.5	22.0	1059	1	CERU_RAT	P13635 rattus norv
35	1684	21.9	1061	2	Q6P5C8_MOUSE	Q6p5c8 mus musculu
36	1644.5	21.4	1062	1	CERU_MOUSE	Q61147 mus musculu
37	1627	21.1	1048	2	Q9XT27_SHEEP	Q9xt27 ovis aries
38	1601.5	20.8	349	2	Q684Q7_MOUSE	Q684q7 mus musculu
39	1599.5	20.8	2102	2	Q7TPK2_RAT	Q7tpk2 rattus norv
40	1589.5	20.7	1007	2	Q4SFU7_TETNG	Q4sfu7 tetraodon n
41	1543.5	20.1	355	2	Q8BQ43_MOUSE	Q8bq43 mus musculu
42	1489.5	19.4	911	2	Q3V1H3_MOUSE	Q3v1h3 mus musculu
43	1443.5	18.8	745	2	Q804X4_CHICK	Q804x4 gallus gall
44	1408	18.3	709	2	Q32PR1_BRARE	Q32pr1 brachydanio
45	1341	17.4	891	2	Q5JUU1_HUMAN	Q5juu1 homo sapien

ALIGNMENTS

RESULT 1

FA8_HUMAN

ID FA8_HUMAN STANDARD; PRT; 2351 AA.
AC P00451;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-FEB-2006, entry version 96.
DE Coagulation factor VIII precursor (Procoagulant component)
DE (Antihemophilic factor) (AHF) [Contains: Factor VIIIa heavy chain, 200
DE kDa isoform; Factor VIIIa heavy chain, 92 kDa isoform; Factor VIII B
DE chain; Factor VIIIa light chain].
GN Name=F8; Synonyms=F8C;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:15:39 ; Search time 198 Seconds
(without alignments)
34.638 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAOSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

```
Database : A_Geneseq_8:*  
1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*\n9: geneseqp2005s:*\n10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query					Description
	Score	Match	Length	DB	ID	
1	75	100.0	15	7	ADM75918	Adm75918 Human MHC
2	75	100.0	15	7	ADM75967	Adm75967 Human MHC
3	75	100.0	15	7	ADM75952	Adm75952 Human MHC
4	75	100.0	15	7	ADM75974	Adm75974 Human Fac
5	75	100.0	15	8	ADG06422	Adg06422 Human B-d
6	75	100.0	20	5	ABJ05003	Abj05003 A3 peptid
7	75	100.0	60	5	ABJ04948	Abj04948 A3 domain
8	75	100.0	642	6	ABP60515	Abp60515 Human fac
9	75	100.0	643	6	ABP60514	Abp60514 Human fac
10	75	100.0	684	2	AAR73022	Aar73022 Human Fac
11	75	100.0	684	2	AAR74091	Aar74091 Factor-VI
12	75	100.0	770	3	ADP20767	Adp20767 Factor VI
13	75	100.0	790	5	ADE64594	Ade64594 Recombina
14	75	100.0	1283	3	AAB07205	Aab07205 Human Fac
15	75	100.0	1284	1	AAP50108	Aap50108 Factor-VI
16	75	100.0	1383	2	AAW33227	Aaw33227 Procoagul
17	75	100.0	1383	2	AAW33228	Aaw33228 Procoagul
18	75	100.0	1383	2	AAW33229	Aaw33229 Procoagul
19	75	100.0	1402	8	ADU47620	Adu47620 Human fac
20	75	100.0	1421	8	ADQ37613	Adq37613 Human Fac
21	75	100.0	1421	8	ADQ37598	Adq37598 Human Fac
22	75	100.0	1422	8	ADQ37591	Adq37591 Human Fac
23	75	100.0	1422	8	ADQ37606	Adq37606 Human Fac
24	75	100.0	1423	8	ADU47614	Adu47614 Human fac
25	75	100.0	1424	1	AAP80268	Aap80268 Modified
26	75	100.0	1424	1	AAP91169	Aap91169 Sequence
27	75	100.0	1424	4	AAB48842	Aab48842 Mutant ma
28	75	100.0	1424	5	AAO18622	Aao18622 Human mat
29	75	100.0	1424	9	ADZ65051	Adz65051 Human mat
30	75	100.0	1425	1	AAP80267	Aap80267 Modified
31	75	100.0	1425	8	ADQ37605	Adq37605 Human Fac
32	75	100.0	1425	8	ADQ37590	Adq37590 Human Fac
33	75	100.0	1426	8	ADU47612	Adu47612 Human fac
34	75	100.0	1428	8	ADQ37599	Adq37599 Human Fac
35	75	100.0	1428	8	ADQ37604	Adq37604 Human Fac
36	75	100.0	1428	8	ADQ37589	Adq37589 Human Fac
37	75	100.0	1428	8	ADQ37614	Adq37614 Human Fac
38	75	100.0	1434	8	ADQ37594	Adq37594 Human Fac
39	75	100.0	1434	8	ADQ37609	Adq37609 Human Fac
40	75	100.0	1435	8	ADQ37600	Adq37600 Human Fac
41	75	100.0	1435	8	ADQ37615	Adq37615 Human Fac
42	75	100.0	1437	8	ADQ37593	Adq37593 Human Fac
43	75	100.0	1437	8	ADQ37608	Adq37608 Human Fac
44	75	100.0	1438	3	AAB01262	Aab01262 B-domain
45	75	100.0	1438	7	ADF31316	Adf31316 Variant o
46	75	100.0	1438	7	ADM75988	Adm75988 Modified
47	75	100.0	1438	7	ADM75985	Adm75985 Modified
48	75	100.0	1438	7	ADM75986	Adm75986 Modified
49	75	100.0	1438	7	ADM75983	Adm75983 Wild-type
50	75	100.0	1438	7	ADM75984	Adm75984 Modified
51	75	100.0	1438	7	ADM75987	Adm75987 Modified
52	75	100.0	1440	2	AAR12971	Aar12971 Factor VI
53	75	100.0	1440	8	ADQ37607	Adq37607 Human Fac
54	75	100.0	1440	8	ADQ37592	Adq37592 Human Fac
55	75	100.0	1441	8	ADQ37612	Adq37612 Human Fac
56	75	100.0	1441	8	ADQ37597	Adq37597 Human Fac
57	75	100.0	1442	8	ADQ37616	Adq37616 Human Fac

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:24:52 ; Search time 51 Seconds
(without alignments)
25.744 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVILRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query				
No.	Score	Match	Length	DB	ID
					Description

1	75	100.0	1438	2	US-09-209-916-1	Sequence 1, Appli
2	75	100.0	1445	2	US-09-407-605-3	Sequence 3, Appli
3	75	100.0	1447	2	US-09-407-605-4	Sequence 4, Appli
4	75	100.0	1457	2	US-09-001-039B-47	Sequence 47, Appli
5	75	100.0	1471	1	US-08-683-839B-3	Sequence 3, Appli
6	75	100.0	1661	1	US-08-882-083-2	Sequence 2, Appli
7	75	100.0	1661	1	US-08-558-107-2	Sequence 2, Appli
8	75	100.0	1661	2	US-09-243-539-2	Sequence 2, Appli
9	75	100.0	2332	1	US-07-864-004B-4	Sequence 4, Appli
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13	75	100.0	2332	1	US-08-474-503-2	Sequence 2, Appli
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21	75	100.0	2332	3	US-10-187-319-2	Sequence 2, Appli
22	75	100.0	2332	3	US-10-131-510A-2	Sequence 2, Appli
23	75	100.0	2332	5	PCT-US93-03275-4	Sequence 4, Appli
24	75	100.0	2332	5	PCT-US94-13200-2	Sequence 2, Appli
25	75	100.0	2351	1	US-08-121-202-2	Sequence 2, Appli
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27	75	100.0	2351	2	US-10-133-907-4	Sequence 4, Appli
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31	69	92.0	2343	2	US-09-324-867-2	Sequence 2, Appli
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33	56	74.7	16	1	US-08-488-379-170	Sequence 170, App
34	56	74.7	16	2	US-08-475-399A-170	Sequence 170, App
35	56	74.7	16	2	US-08-077-255A-170	Sequence 170, App
36	56	74.7	16	5	PCT-US93-07545-170	Sequence 170, App
37	56	74.7	868	1	US-07-864-004B-6	Sequence 6, Appli
38	56	74.7	868	1	US-08-251-937A-6	Sequence 6, Appli
39	56	74.7	868	1	US-08-212-133A-3	Sequence 3, Appli
40	56	74.7	1090	5	PCT-US93-03275-6	Sequence 6, Appli
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42	56	74.7	1443	2	US-09-037-601-39	Sequence 39, Appl
43	56	74.7	1443	2	US-09-315-179-39	Sequence 39, Appl
44	56	74.7	1443	3	US-10-187-319-39	Sequence 39, Appl
45	56	74.7	1443	3	US-10-131-510A-39	Sequence 39, Appl
46	56	74.7	1467	2	US-09-523-656-38	Sequence 38, Appl
47	56	74.7	2115	2	US-09-324-867-5	Sequence 5, Appli
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51	56	74.7	2133	2	US-09-523-656-30	Sequence 30, Appl
52	56	74.7	2133	3	US-10-187-319-37	Sequence 37, Appl
53	56	74.7	2133	3	US-10-131-510A-37	Sequence 37, Appl
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59	43	57.3	2319	2	US-09-315-179-6	Sequence 6, Appli
60	43	57.3	2319	2	US-09-523-656-28	Sequence 28, Appl

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:36:35 ; Search time 180 Seconds
(without alignments)
38.601 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	75	100.0	20	4	US-10-433-273-59	Sequence 59, Appl
4	75	100.0	60	4	US-10-433-273-4	Sequence 4, Appli
5	75	100.0	1424	5	US-10-472-516-5	Sequence 5, Appli
6	75	100.0	1424	5	US-10-968-286-5	Sequence 5, Appli
7	75	100.0	1438	4	US-10-006-091-1	Sequence 1, Appli
8	75	100.0	1438	4	US-10-047-257-1	Sequence 1, Appli
9	75	100.0	1438	4	US-10-225-900-1	Sequence 1, Appli
10	75	100.0	1438	5	US-10-511-559-73	Sequence 73, Appl
11	75	100.0	1457	5	US-10-813-507-13	Sequence 13, Appl
12	75	100.0	1457	5	US-10-813-507-17	Sequence 17, Appl
13	75	100.0	1459	4	US-10-239-498A-4	Sequence 4, Appli
14	75	100.0	1459	4	US-10-239-498A-13	Sequence 13, Appl
15	75	100.0	1459	4	US-10-239-498A-15	Sequence 15, Appl
16	75	100.0	1471	4	US-10-095-718-2	Sequence 2, Appli
17	75	100.0	1471	4	US-10-681-970-2	Sequence 2, Appli
18	75	100.0	2096	5	US-10-741-600-1032	Sequence 1032, Ap
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20	75	100.0	2332	3	US-09-957-641-2	Sequence 2, Appli
21	75	100.0	2332	4	US-10-187-319-2	Sequence 2, Appli
22	75	100.0	2332	4	US-10-131-510A-2	Sequence 2, Appli
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28	75	100.0	2332	4	US-10-721-997A-34	Sequence 34, Appl
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34	75	100.0	2351	4	US-10-132-829-4	Sequence 4, Appli
35	75	100.0	2351	4	US-10-172-712-27	Sequence 27, Appl
36	75	100.0	2351	4	US-10-133-907-4	Sequence 4, Appli
37	75	100.0	2351	4	US-10-411-037-30	Sequence 30, Appl
38	75	100.0	2351	4	US-10-411-026-30	Sequence 30, Appl
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41	75	100.0	2351	4	US-10-410-930-30	Sequence 30, Appl
42	75	100.0	2351	4	US-10-410-997-30	Sequence 30, Appl
43	75	100.0	2351	4	US-10-411-012-30	Sequence 30, Appl
44	75	100.0	2351	4	US-10-287-994-30	Sequence 30, Appl
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48	75	100.0	2351	5	US-10-741-600-1034	Sequence 1034, Ap
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52	75	100.0	2351	5	US-10-492-261-30	Sequence 30, Appl
53	75	100.0	2351	5	US-10-995-561-608	Sequence 608, App
54	75	100.0	2351	6	US-11-183-205-30	Sequence 30, Appl
55	75	100.0	2351	6	US-11-244-087-3	Sequence 3, Appli
56	75	100.0	2351	6	US-11-267-631-49	Sequence 49, Appl
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58	69	92.0	1431	4	US-10-681-970-4	Sequence 4, Appli
59	65	86.7	13	5	US-10-511-559-831	Sequence 831, App
60	64	85.3	13	5	US-10-511-559-832	Sequence 832, App
61	58	77.3	13	5	US-10-511-559-833	Sequence 833, App

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:36:39 ; Search time 15 Seconds
(without alignments)
11.137 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831

Perfect score: 75

Sequence: 1 MSSSPHVLRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:
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3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	75	100.0	2351	7 US-11-280-757-35	Sequence 35, Appl
4	38	50.7	245	6 US-10-953-349-37574	Sequence 37574, A
5	38	50.7	462	6 US-10-953-349-32051	Sequence 32051, A
6	37	49.3	862	6 US-10-199-229-14	Sequence 14, Appl
7	37	49.3	875	6 US-10-199-229-10	Sequence 10, Appl
8	37	49.3	1167	7 US-11-121-154-1	Sequence 1, Appl
9	36	48.0	165	6 US-10-953-349-38626	Sequence 38626, A
10	35	46.7	234	6 US-10-953-349-33666	Sequence 33666, A
11	35	46.7	240	6 US-10-953-349-16702	Sequence 16702, A
12	35	46.7	273	6 US-10-953-349-33665	Sequence 33665, A
13	35	46.7	356	6 US-10-953-349-33664	Sequence 33664, A
14	35	46.7	374	6 US-10-953-349-2190	Sequence 2190, Ap
15	35	46.7	380	6 US-10-953-349-2189	Sequence 2189, Ap
16	35	46.7	460	6 US-10-953-349-32416	Sequence 32416, A
17	35	46.7	517	6 US-10-953-349-32415	Sequence 32415, A
18	35	46.7	558	6 US-10-953-349-32414	Sequence 32414, A
19	35	46.7	1807	6 US-10-504-120-22	Sequence 22, Appl
20	34	45.3	190	6 US-10-953-349-26757	Sequence 26757, A
21	34	45.3	230	6 US-10-953-349-26790	Sequence 26790, A
22	34	45.3	251	6 US-10-953-349-26789	Sequence 26789, A
23	34	45.3	365	6 US-10-953-349-331	Sequence 331, App
24	34	45.3	376	6 US-10-953-349-330	Sequence 330, App
25	34	45.3	385	6 US-10-953-349-423	Sequence 423, App
26	34	45.3	386	6 US-10-953-349-13553	Sequence 13553, A
27	34	45.3	386	6 US-10-953-349-17965	Sequence 17965, A
28	34	45.3	392	6 US-10-953-349-422	Sequence 422, App
29	34	45.3	393	6 US-10-953-349-329	Sequence 329, App
30	34	45.3	409	6 US-10-953-349-421	Sequence 421, App
31	34	45.3	417	6 US-10-953-349-13552	Sequence 13552, A
32	34	45.3	417	6 US-10-953-349-17964	Sequence 17964, A
33	34	45.3	777	7 US-11-293-697-3189	Sequence 3189, Ap
34	34	45.3	1237	7 US-11-325-764-32	Sequence 32, Appl
35	33.5	44.7	205	6 US-10-953-349-15363	Sequence 15363, A
36	33.5	44.7	206	6 US-10-953-349-28535	Sequence 28535, A
37	33	44.0	188	6 US-10-953-349-36581	Sequence 36581, A
38	33	44.0	194	6 US-10-953-349-2806	Sequence 2806, Ap
39	33	44.0	205	7 US-11-293-697-4682	Sequence 4682, Ap
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44	33	44.0	301	6 US-10-953-349-6479	Sequence 6479, Ap
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47	33	44.0	309	6 US-10-953-349-6478	Sequence 6478, Ap
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53	33	44.0	334	6 US-10-953-349-15723	Sequence 15723, A
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57	33	44.0	368	6 US-10-953-349-21272	Sequence 21272, A
58	33	44.0	425	6 US-10-953-349-20579	Sequence 20579, A
59	33	44.0	461	6 US-10-953-349-20578	Sequence 20578, A

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A;Cross-references: UNIPROT:O86332; UNIPARC:UPI00000C1598; GB:Z80226; GB:AL123456; NII C;Species: Synechocystis sp. A;Variety: PCC 6803 C;Date: 25-Apr-1997 #sequence_revision 25-A| cyanobacterium Synechocystis sp. PCC6803. II. Sequence determination of the entire genome and the EMBL Data Library, June 1996 C;Genetics: A;Gene: dnaJ A;Start codon: GTG F;24-91/Domain: 1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004 C;Accession: S46093 R;Dubois, SGD:APG12; MIPS:YBR217w A;Cross-references: SGD:S0000421 A;Map position: 2R C;Superfamil OHP1b C;Species: Zea mays (maize) C;Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #tex UNIPARC:UPI00000A9ACE; GB:U35063; NID:g1144535; PIDN: AAC49533.1; PID:g1144536 C;Com SSPHVLQN 176 RESULT 20 E84504 hypothetical protein At2g12910 [imported] - Arabidopsis thalia Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Pre PIDN:AAD20650.1; GSPDB:GN00139 C;Genetics: A;Gene: At2g12910 A;Map position: 2 C;Superfa C;Accession: A54277; S60344 R;Eckner, R.; Ewen, M.E.; Newsome, D.; Gerdes, M.; DeCaprio, J.A GB:U01877; NID:g495300; PIDN:AAA18639.1; PID:g495301 A;Note: in the authors' translation 9< 552-660 A;Cross-references: UNIPARC:UPI00001782EB C;Genetics: A;Gene: GDB:EP300 A;Cross-(covalent) (by protein kinase A) #status predicted Query Match 50.7%; Score 38; DB 2; Length 24 Goodman, R.H. Nature 365, 855-859, 1993 A;Title: Phosphorylated CREB binds specifically to the r Score 38; DB 2; Length 2441; Best Local Similarity 57.1%; Pred. No. 2.9e+02; Matches 8; Conser Nagai, Y.; Lian, J.; Ito, T.; Kanamori, M.; Matsumaru, H.; Maruyama, A.; Murakami, H.; Hosoyama G89787 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-698 A;Cross-references: UNIPF T15D22.1 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Ma Goldsmith, A.D.; Haas, B.; Hansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Autl Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; To NID:g6899642; PIDN:AAF31019.1; GSPDB:GN00141 C;Genetics: A;Map position: 1 Query Match 4 Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, H.; Brandt, P.; Chakrat G.; Novella, S.; de Pablos, B.; Perez-Diaz, J.C.; Remmel, B.; Rose, M.; Rusniok, C.; Schlueter, T.; C;Genetics: A;Gene: ImAC Query Match 49.3%; Score 37; DB 2; Length 138; Best Local Similarity Sebaihia, M.; James, K.D.; Churcher, C.; Mungall, K.L.; Baker, S.; Basham, D.; Bentley, S.D.; Broo PMID:11586360 A;Accession: AG0335 A;Status: preliminary A;Molecule type: DNA A;Residues: 1- HLLRQRAQCG 352 RESULT 27 G89902 competence-damage inducible protein cinA [imported] - Sta K.; Hirakawa, H.; Kuhara, S.; Goto, S.; Yabuzaki, J.; Kanehisa, M.; Yamashita, A.; Oshima, K.; Fur PIDN:BAB42379.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics: A;Gene: cin/ Alcaligenes latus C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-200 A;Cross-references: UNIPROT:Q9ZGI9; UNIPARC:UPI00000B22B2; EMBL:AF078795; PIDN: AAC836 elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-199 CESP:F08C6.3 A;Experimental source: strain Bristol N2 C;Genetics: A;Gene: CESPF08C6.3 A;Intr thaliana (mouse-ear cress) A;Variety: columbia C;Date: 03-Aug-1998 #sequence_revision 03-Aug- Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B. Nature 391, 485-488, 199 sequence from chromosome 4 of Arabidopsis thaliana. A;Reference number: A71400; MUID:98121 45.5%; Pred. No. 1.8e+02; Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0; Qy 1 MSS K.F.X. submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24460 A;Ac Indels 0; Gaps 0; Qy 4 SPHVLRNRAQ 13 :||:| |||: Db 920 APHLLENRAR 929 RESULT 32 T33123 hy type: DNA A;Residues: 1-2275 A;Cross-references: UNIPARC:UPI000017B6FD; EMBL:AF067608; F 70.0%; Pred. No. 4.1e+02; Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0; Qy 5 PHv Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequer acetyltransferase Query Match 48.7%; Score 36.5; DB 2; Length 394; Best Local Similarity 55.6%. B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; I

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:19:54 ; Search time 38 Seconds
(without alignments)
37.980 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAOSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	75	100.0	2351	1	EZHU	coagulation factor
2	56	74.7	869	2	A25945	coagulation factor
3	56	74.7	2133	2	T42763	coagulation factor
4	50	66.7	440	2	G82426	probable phosphogl
5	43	57.3	2319	2	A47004	coagulation factor
6	42	56.0	355	1	S22181	gamma-1-microglobu
7	40	53.3	133	2	JC7103	endo-1,4-beta-xyla
8	40	53.3	390	2	F83220	hypothetical prote
9	40	53.3	584	2	H95336	probable adenylate
10	40	53.3	616	2	B33586	C4-dicarboxylate t
11	40	53.3	621	2	D96032	C4-dicarboxylate t
12	39	52.0	88	2	C84469	hypothetical prote
13	39	52.0	312	2	B86494	integrase/recombin
14	39	52.0	312	2	F72129	integrase/recombin
15	39	52.0	443	2	I38603	heme A farnesyltra
16	38	50.7	101	2	D70710	hypothetical prote
17	38	50.7	174	2	S74666	DnAJ protein - Syn
18	38	50.7	186	2	S46093	probable membrane
19	38	50.7	405	2	JC5175	seed storage prote
20	38	50.7	567	2	E84504	hypothetical prote
21	38	50.7	2414	2	A54277	transcription adap
22	38	50.7	2441	2	S39161	CREB-binding prote
23	37.5	50.0	698	2	G89787	hypothetical prote
24	37	49.3	133	2	A86283	hypothetical prote
25	37	49.3	138	2	AE1089	Antigen C homolog
26	37	49.3	361	2	AG0335	chorismate synthas
27	37	49.3	383	2	G89902	competence-damage
28	37	49.3	392	2	T51772	acetyl-CoA C-acety
29	37	49.3	650	2	T15972	hypothetical prote
30	37	49.3	1052	2	E71422	hypothetical prote
31	37	49.3	1256	2	T47325	hypothetical prote
32	37	49.3	2275	2	T33123	hypothetical prote
33	36.5	48.7	394	2	E65067	hypothetical prote
34	36.5	48.7	394	2	H85936	probable acyltrans
35	36.5	48.7	394	2	E91091	probable acyltrans
36	36	48.0	62	2	S44153	hypothetical prote

SCORE Search Results Details for Application 10511559 and Search Result us-10-511-559- 73_copy_817_831.rup.

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OM protein - protein search, using sw model

Run on: May 25, 2006, 11:15:52 ; Search time 296 Seconds
(without alignments)
46.876 Million cell updates/sec

Title: US-10-511-559-73_COPY_817_831
Perfect score: 75
Sequence: 1 MSSSPHVLRNRAQSG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*

```

1: uniprot_sprot:*
2: uniprot_trembl:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	% Match Length DB ID				Description
		1	2	3	4	
1	75	100.0	2351	1	FA8_HUMAN	P00451 h coagulati
2	75	100.0	2351	2	Q5HY69_HUMAN	Q5hy69 homo sapien
3	69	92.0	2343	1	FA8_CANFIA	O18806 canis famil
4	56	74.7	2133	1	FA8_PIG	P12263 sus scrofa

5	50	66.7	313	2	Q5DBY4_SCHJA	Q5dby4 schistosoma
6	50	66.7	440	2	Q9KLN7_VIBCH	Q9kln7 vibrio chol
7	49	65.3	288	2	Q5LLG7_SILPO	Q5llg7 silicibacte
8	46	61.3	332	2	Q55R49_CRYNE	Q55r49 cryptococco
9	46	61.3	355	2	Q5KF20_CRYNE	Q5kf20 cryptococco
10	44	58.7	473	2	Q3CGK8_THEET	Q3cgk8 thermoanaer
11	43	57.3	282	2	Q3JWP8_BURP1	Q3jwp8 burkholderi
12	43	57.3	282	2	Q62MY6_BURMA	Q62my6 burkholderi
13	43	57.3	282	2	Q63Y07_BURPS	Q63y07 burkholderi
14	43	57.3	290	2	Q7VZE1_BORPE	Q7vze1 bordetella
15	43	57.3	290	2	Q7WGW7_BORBR	Q7wgw7 bordetella
16	43	57.3	597	2	Q420I1_DESHA	Q420i1 desulfitoba
17	43	57.3	2319	1	FA8_MOUSE	Q06194 mus musculu
18	42	56.0	206	2	Q5Z752_ORYSA	Q5z752 oryza sativ
19	42	56.0	355	1	AMBP_PLEPL	P36992 pleuronecte
20	42	56.0	382	2	Q36R03_MARHY	Q36r03 marinobacte
21	42	56.0	399	2	Q485V8_COLP3	Q485v8 colwellia p
22	42	56.0	827	2	Q4R3D7_MACFA	Q4r3d7 macaca fasc
23	42	56.0	1742	2	Q32WC7_9VIRU	Q32wc7 dulcamara m
24	41	54.7	139	2	Q2J3U5_RHOPA	Q2j3u5 rhodopseudo
25	41	54.7	349	2	Q8D3B4_WIGBR	Q8d3b4 wiggleswort
26	41	54.7	366	2	Q31FE3_THICR	Q31fe3 thiomicrosp
27	41	54.7	1155	2	Q54NV0_DICDI	Q54nv0 dictyosteli
28	41	54.7	1846	2	Q4WU73_ASPFU	Q4wu73 aspergillus
29	40	53.3	69	2	Q6K254_ORYSA	Q6k254 oryza sativ
30	40	53.3	133	2	Q9Z490_9BACI	Q9z490 bacillus sp
31	40	53.3	160	1	RUVX_GLUOX	Q5fnl1 gluconobact
32	40	53.3	166	2	Q6IGV6_DROME	Q6igv6 drosophila
33	40	53.3	254	2	Q2R8P0_ORYSA	Q2r8p0 oryza sativ
34	40	53.3	356	2	Q86865_STRGA	Q86865 streptomyce
35	40	53.3	390	2	Q9HYK3_PSEAE	Q9hyk3 pseudomonas
36	40	53.3	405	2	Q46TI9_RALEJ	Q46ti9 ralstonia e
37	40	53.3	423	2	Q3RWW9_RALME	Q3rww9 ralstonia m
38	40	53.3	439	2	Q820M8_NITEU	Q820m8 nitrosomona
39	40	53.3	462	2	Q3FC44_9BURK	Q3fc44 burkholderi
40	40	53.3	462	2	Q44U36_9BURK	Q44u36 burkholderi
41	40	53.3	462	2	Q4LJ36_9BURK	Q4lj36 burkholderi
42	40	53.3	462	2	Q394B7_BURS3	Q394b7 burkholderi
43	40	53.3	472	2	Q5ZR27_CAEEL	Q5zr27 caenorhabdi
44	40	53.3	584	2	Q92Z92_RHIME	Q92z92 rhizobium m
45	40	53.3	621	1	DCTB_RHIME	P13633 rhizobium m
46	40	53.3	642	2	Q4X104_ASPFU	Q4x104 aspergillus
47	40	53.3	711	2	Q6D6D1_ERWCT	Q6d6d1 erwinia car
48	40	53.3	846	2	Q38AP3_9TRYP	Q38ap3 trypanosoma
49	40	53.3	863	2	Q73D59_BACC1	Q73d59 bacillus ce
50	40	53.3	1241	2	Q57WH0_9TRYP	Q57wh0 trypanosoma
51	40	53.3	1823	2	Q90Z25_9TELE	Q90z25 sternopygus
52	40	53.3	2473	2	Q4SSB2_TETNG	Q4ssb2 tetraodon n
53	39.5	52.7	915	2	Q4P1S8_USTMA	Q4pls8 ustilago ma
54	39	52.0	88	2	Q9SL17_ARATH	Q9s117 arabidopsis
55	39	52.0	136	2	Q3SET3_THIDA	Q3set3 thiobacillu
56	39	52.0	141	2	Q6Z5C7_ORYSA	Q6z5c7 oryza sativ
57	39	52.0	208	2	Q6FT33_CANGA	Q6ft33 candida gla
58	39	52.0	275	2	Q3FAV9_9BURK	Q3fav9 burkholderi
59	39	52.0	282	2	Q2T1N7_BURTH	Q2t1n7 burkholderi
60	39	52.0	288	2	Q3IXE7_RHOS4	Q3ixe7 rhodobacter
61	39	52.0	297	2	Q72TM1_LEPIC	Q72tm1 leptospira
62	39	52.0	297	2	Q8F1M8_LEPIN	Q8f1m8 leptospira
63	39	52.0	312	1	XERC_CHLPN	Q9z9f7 chlamydia p
64	39	52.0	349	2	Q2X6P3_9GAMM	Q2x6p3 shewanella
65	39	52.0	349	2	Q2ZAQ5_9GAMM	Q2zaq5 shewanella